

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:59 ; Search time 32.09 Seconds  
(without alignments)  
337.077 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742  
Sequence: 1 MAVLVFLCLVAPPCVLSQ.....MKRGYAMDYWGQGLTVTVSS 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
al number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	588.5	79.3	141	2 S52446	Ig heavy chain V r
2	561.5	75.7	139	2 A32456	Ig heavy chain pre
3	558	75.2	140	2 S55028	Ig heavy chain V r
4	528.5	71.2	135	2 S31913	Ig gamma-2A chain
5	525	70.8	117	2 S10111	Ig heavy chain V r
6	510	68.7	140	2 S14238	Ig gamma-1 chain p
7	506	68.2	144	1 G2MS14	Ig gamma-2a chain
8	504.5	66.2	140	2 I37782	Ig variable region
9	491	66.2	140	2 S11244	Ig heavy chain V r
10	483.5	65.2	137	2 S31676	Ig heavy chain V r
11	481.5	64.9	120	2 PL0087	Ig heavy chain V r
12	481.5	64.9	139	2 S31586	Ig heavy chain V r
13	478	64.4	116	2 S33952	Ig heavy chain V r
14	478	64.4	155	2 S33952	Ig mu chain precu
15	476	64.2	147	2 S15111	Ig heavy chain - h
16	475	64.0	116	2 S13519	Ig heavy chain V r
17	475	64.0	155	2 S31512	Ig heavy chain pre
18	469	63.2	112	2 S11100	Ig heavy chain - h
19	467.5	63.0	145	2 S78055	Ig heavy chain V r
20	467	62.9	130	2 S31690	Ig heavy chain pre
21	466	62.8	114	2 S11106	Ig heavy chain V r
22	464	62.5	115	2 S11106	Ig heavy chain V r
23	464	62.5	115	1 HVMS14	Ig heavy chain pre
24	464	62.5	116	2 S11102	Ig heavy chain V r
25	464	62.5	127	2 B31807	Ig heavy chain V r
26	459	61.9	146	2 S09711	Ig heavy chain V r
27	458	61.7	118	2 P00266	Ig heavy chain V r
28	456.5	61.5	117	2 S38563	Ig heavy chain V r
29	456	61.5	146	2 S09710	Ig heavy chain V r

30 454 61.2 139 2 S31696  
31 453 61.1 140 2 A49045  
32 450.5 60.7 116 2 S42484  
33 449 60.5 114 2 S11099  
34 449 60.5 115 2 S11103  
35 449 60.5 115 2 S26322  
36 447 60.2 106 2 S11108  
37 446 60.1 135 2 S78051  
38 444.5 59.9 118 2 S32786  
39 444 59.8 121 2 S33131  
40 442.5 59.6 140 2 S78052  
41 441 59.4 114 2 S26321  
42 441 59.4 140 2 S54239  
43 441 59.4 144 2 S54244  
44 439 59.2 121 2 D30560  
45 438.5 59.1 141 2 S54236

## ALIGNMENTS

### RESULT 1

S52446

Ig heavy chain V region precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 23-Jul-1999

C:Accession: S52446

R:Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A:Description: Specific amplification by the polymerase chain reaction of rearranged

A:Reference number: S52445

A:Accession: S52446

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-141 <BER>

A:Cross-references: EMBL:X82692; NID:9673441; PIDN:CAA58013.1; PID:9673442

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 588.5; DB 2; Length 141;  
Best Local Similarity 81.0%; Pred. No. 7e-45;  
Matches 115; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 MAVLVFLCLVAPPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60

Db 1 MAVLVFLCLVAPPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60

QY 61 GKLEWLGVIWAGGTTNNYNSALMSRLTTSKDTSKNOVSKLSSVTAADTAVYVCARGPPH 120

Db 61 GKLEWLGVIWAGGTTNNYNSALMSRLTTSKDTSKNOVSKLSSVTAADTAVYVCARGPPH 120

QY 121 AMMKRGYAMDYWGQGLTVTVSS 142

Db 120 STMDTPYAMDYWGQGLTVTVSS 141

### RESULT 2

A32456

Ig heavy chain precursor V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 26-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 23-Jul-1999

C:Accession: A32456

R:Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.

J. Biol. Chem. 264, 4513-4522, 1989

A:Title: Variable region primary structures of a high affinity anti-fluorescein immu

A:Reference number: A32456; MOID:89174706

A:Accession: A32456

A:Status: preliminary

A:Molecule type: mRNA

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A;Residues: 1-135 <BES>  
A;Cross-references: EMBL:X70822; NID:g57921; PIDN:CAA50153.1; PID:g57922  
A;Experimental source: strain BALB/c  
C;Superfamily: immunoglobulin V region; immunoglobulin  
C;Keywords: heterotetramer; immunoglobulin  
F;1-11/Domain: signal sequence #status predicted <SIG>  
F;12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 528.5; DB 2; Length 135;  
Best Local Similarity 70.4%; Pred. No. 1.2e-39; Indels 7; Gaps 1;  
Matches 100; Conservative 19; Mismatches 16;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
Db 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQSP 60  
QY 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCARGPPH 120  
Db 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCAR---- 116  
QY 121 AMKRGYAMDYWGQGLTVTVSS 142  
Db 117 --ELVYFYDYWGQGLTVTVSS 135

RESULT 5

S10111  
Ig heavy chain V region (clone 26) precursor - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S10111  
R;Kaartinen, M.; Solin, M.L.; Maekelae, O.  
EMBO J. 8, 1743-1748, 1989  
A;Title: 'Allelic' forms of immunoglobulin V genes in different strains of mice.  
A;Reference number: S10111; MUID:89356648  
A;Accession: S10111  
A;Molecule type: mRNA  
A;Residues: 1-117 <KAA>  
A;Cross-references: EMBL:X15471; NID:g50005; PIDN:CAA33499.1; PID:g50006  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 525; DB 2; Length 117;  
Best Local Similarity 85.3%; Pred. No. 2.2e-39;  
Matches 99; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
Db 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
QY 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCAR 116  
Db 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCAR 116

RESULT 6

S14238  
Ig gamma-1 chain precursor (15C5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S14238  
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.  
Eur. J. Biochem. 192, 767-775, 1990  
A;Title: Construction and characterization of a recombinant murine monoclonal antibody  
A;Reference number: S14236; MUID:91006173  
A;Accession: S14238  
A;Molecule type: mRNA  
A;Residues: 1-140 <VAN>  
A;Cross-references: EMBL:X56392; NID:g51619; PIDN:CAA39803.1; PID:g747853

A;Residues: 1-139 <DOM>  
A;Cross-references: GB:J04609; NID:g556316; PIDN:AAA50298.1; PID:g556317  
A;Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 561.5; DB 2; Length 139;  
Best Local Similarity 76.4%; Pred. No. 1.6e-42; Indels 7; Gaps 2;  
Matches 110; Conservative 14; Mismatches 13;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
Db 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
QY 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCARGPPH 120  
Db 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCAK---- 116  
QY 121 AMKRGYAMDYWGQGLTVTVSS 142  
Db 117 -RLERIFYAMDYWGQGLTVTVSS 139

RESULT 3

S55028  
Ig heavy chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 23-Jul-1999  
C;Accession: S55028  
R;Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff,  
J. Mol. Biol. 248, 344-360, 1995  
A;Title: Structure and specificity of the anti-digoxin antibody 40-50.  
A;Reference number: S55027; MUID:95257394  
A;Accession: S55028  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140 <JEF>  
A;Cross-references: EMBL:L31403; NID:g476717; PIDN:AAA38191.1; PID:g476718  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 558; DB 2; Length 140;  
Best Local Similarity 76.1%; Pred. No. 3.3e-42;  
Matches 108; Conservative 15; Mismatches 17; Indels 2; Gaps 1;

QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
Db 1 MAVLVFLCLVAFPCVLSQVQLQESGPGVLPKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60  
QY 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCARGPPH 120  
Db 61 GKLEWLGVIWAGGTTNYSALMSRLTISKDTSKNOVSLKLSSTAAADTAVYYCARF--R 118

RESULT 4

S31913  
Ig gamma-2A chain precursor - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 23-Jul-1999  
C;Accession: S31913  
R;Bespalov, I.A.; Hiyonov, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova  
submitted to the EMBL data library, January 1993  
A;Reference number: S31913  
A;Accession: S31913  
A;Molecule type: mRNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:26-108/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 510; DB 2; Length 140;  
Best Local Similarity 70.1%; Pred. No. 5.4e-38;  
Matches 94; Conservative 21; Mismatches 13; Indels 6; Gaps 1;  
QY 9 CLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPPGKLEWLG 68  
DB 1 CLVTFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPPGKLEWLG 60  
QY 69 VIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPPHAMKRGYA 128  
DB 61 VIWSGSTYDYNAAFTSLRSLINKNSQVQFKNLSQANDTAIYYCARN-----YWGTS 114  
QY 129 MDYWGQGTSLTVTVSS 142  
DB 115 MDYWGQGTSLTVTVSS 128

RESULT 7  
G2MS14  
Ig heavy chain precursor V region (MOPC 141) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Oct-1980 #sequence\_revision 31-Oct-1980 #text\_change 16-Jun-2000  
C:Accession: A02094  
R:Sakano, H.; Maki, R.; Kurosawa, Y.; Roeder, W.; Tonegawa, S.  
Nature 286, 676-683, 1980  
A:Title: Two types of somatic recombination are necessary for the generation of complete  
A:Reference number: A03229; MUID:81012133  
A:Accession: A02094  
A:Molecule type: DNA  
A:Residues: 1-144 <SAK>  
A:Cross-references: GB:V00768; GB:J00491; NID:g51615; PIDN:CAA24149.1; PID:g51616  
A:Note: the sequence shown was determined from a differentiated gene isolated from a myeloma cell line. The sequence shown was determined from a myeloma cell line. The sequence shown was determined from a myeloma cell line.  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-144/Product: Ig heavy chain V region (MOPC 141) #status predicted <MAT>  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 506; DB 1; Length 144;  
Best Local Similarity 67.4%; Pred. No. 1.3e-37;  
Matches 97; Conservative 15; Mismatches 30; Indels 2; Gaps 1;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
DB 1 MAVLALLFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
QY 61 GKLEWLGVIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPP 118  
DB 61 GKLEWLGVIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPP 120  
QY 119 PHAMKRGYAMDYWGQGTSLTVTVSS 142  
DB 121 YGSRSDKYFTLDYWGQGTSLTVTVSS 144

RESULT 8  
S11244  
Ig gamma-2a chain precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S11244  
R:Wellman, A.A.; Meares, C.F.  
Nucleic Acids Res. 18, 5281, 1990  
A:Title: Sequences of the Lyn-1 antibody heavy and light chain variable regions.

A:Reference number: S11244; MUID:90384832  
A:Accession: S11244  
A:Molecule type: mRNA  
A:Residues: 1-144 <WEL>  
A:Cross-references: EMBL:X53483  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 504.5; DB 2; Length 144;  
Best Local Similarity 70.4%; Pred. No. 1.7e-37;  
Matches 100; Conservative 15; Mismatches 22; Indels 5; Gaps 2;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
DB 1 MAVLGLLLCLVTFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
QY 61 GKLEWLGVIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPPH 120  
DB 61 GKLEWLVVWSDGTTYNALSKRLSISKNSKSOVFLKMNLSLQTDITAIYYCA---SH 117  
QY 121 AMMKRGYAMDYWGQGTSLTVTVSS 142  
DB 118 YGSLTAFAS--WGHGTLTVTSA 137

RESULT 9  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed b  
A:Reference number: A36876; MUID:94119917  
A:Accession: I37782  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 491; DB 2; Length 140;  
Best Local Similarity 71.8%; Pred. No. 2.5e-36;  
Matches 102; Conservative 11; Mismatches 27; Indels 2; Gaps 1;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
DB 1 MKHLWFFLLVLAAPRWVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYVYVRRQPP 60  
QY 61 GKLEWLGVIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPPH 120  
DB 61 GKLEWLGVIWAGTNNYNSALMSRLTISKDTSKNOVSLKSSVTAAATVAVYCARPPH 120  
QY 121 AMMKRGYAMDYWGQGTSLTVTVSS 142  
DB 121 SWYGRYF--DYWGQGTSLTVTVSS 140

RESULT 10  
S31676  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31676  
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t  
A:Reference number: S31585

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A:Description: Mechanisms that generate human immunoglobulin diversity operate from t  
A:Reference number: S31585  
A:Accession: S31586  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 483.5; DB 2; Length 137;  
Best Local Similarity 71.1%; Pred. No. 1.1e-35; Indels 5; Gaps 2;  
Matches 101; Conservative 11; Mismatches 25;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWRQPP 60  
Db 1 MKHLNFFLLVAAPRWLSQVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPA 60  
QY 61 GKGLWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPH 120  
Db 61 GKGLWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPH 120  
QY 61 GKLEWIGRIYTSSTNYPNPSLKRVTMSVDTSKNQFSLKSSVTAADTAVYYCARDAP- 119  
Db 61 GKLEWIGRIYTSSTNYPNPSLKRVTMSVDTSKNQFSLKSSVTAADTAVYYCARDAP- 119  
QY 121 AMKRGYAMDYWGQGLTVTVSS 142  
Db 121 AMKRGYAMDYWGQGLTVTVSS 137  
QY 120 -LM---YGMVWGQGLTVTVSS 137  
Db 120 -LM---YGMVWGQGLTVTVSS 137

RESULT 11  
A33932  
Ig mu chain precursor V region (D23) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 23-Jul-1999  
C:Accession: PLO087  
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A:Title: Structural characterization of antidiotopic antibodies; evidence that Ab2s are  
A:Reference number: PLO080; MUID:89094248  
A:Accession: PLO087  
A:Molecule type: mRNA  
A:Residues: 1-120 <ME>  
A:Cross-references: GB:X58593; GB:Y00794; NID:g51571; PIDN:CAA1468.1; PID:g938252  
A:Experimental source: strain BALB/C  
A:Note: the sequence shown here is from the VH region of an antidiotopic monoclonal ant  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 481.5; DB 2; Length 120;  
Best Local Similarity 75.6%; Pred. No. 1.5e-35; Indels 1;  
Matches 93; Conservative 12; Mismatches 15;  
QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWRQPPGKGLWGLVWAGGTTNN 79  
Db 1 QVQLKRSGLVAPQSLSITCTVSGFSLTSYGYYVWRQPPGKGLWGLVWAGGTTNN 60  
QY 80 SALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPHAMKRGYAMDYWGQGLTVT 139  
Db 61 SALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPHAMKRGYAMDYWGQGLTVT 117  
QY 140 VSS 142  
Db 118 VSS 120

RESULT 12  
S31586  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31586  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992

Query Match 64.9%; Score 481.5; DB 2; Length 139;  
Best Local Similarity 71.1%; Pred. No. 1.7e-35; Indels 3; Gaps 2;  
Matches 101; Conservative 13; Mismatches 25;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWRQPP 60  
Db 1 MKHLNFFLLVAAPRWLSQVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPA 60  
QY 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPH 120  
Db 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCARGPPH 120  
QY 61 GKLEWIGRIYTSSTNYPNPSLKRVTMSVDTSKNQFSLKSSVTAADTAVYYCARDAP- 118  
Db 61 GKLEWIGRIYTSSTNYPNPSLKRVTMSVDTSKNQFSLKSSVTAADTAVYYCARDAP- 118  
QY 121 AMKRGYAMDYWGQGLTVTVSS 142  
Db 121 AMKRGYAMDYWGQGLTVTVSS 139  
QY 119 LGIRRG-AFDINGQGTMTVTVSS 139  
Db 119 LGIRRG-AFDINGQGTMTVTVSS 139

RESULT 13  
A33932  
Ig mu chain precursor V region (D23) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1990 #sequence\_revision 18-Sep-1992 #text\_change 23-May-1997  
C:Accession: A33932  
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A:Title: Two murine natural polyclonal autoantibodies are encoded by nonmutated ger  
A:Reference number: A33932; MUID:89282823  
A:Accession: A33932  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <BA>  
A:Cross-references: GB:M27107  
A:Note: the authors translated the codon CTA for residue 18 as Thr  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 478; DB 2; Length 116;  
Best Local Similarity 75.9%; Pred. No. 2.9e-35; Indels 0; Gaps 0;  
Matches 88; Conservative 17; Mismatches 11;  
QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWRQPP 60  
Db 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWRQPP 60  
QY 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116  
Db 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116  
QY 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116  
Db 61 GKLEWGLVWAGGTTNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116

RESULT 14  
S31511  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31511  
R:Chastagner, P.; Demaison, C.; There, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a  
A:Reference number: S31509

Query Match	64.4%;	Score 478;	DB 2;	Length 155;
Best Local Similarity	69.7%;	Pred. No. 3.9e-35;		
Matches 99;	Conservative 10;	Mismatches 33;	Indels 0;	Gaps 0;

  

QY	1	M	A	V	L	V	L	F	L	C	I	A	P	P	S	C	V	L	S	O	V	L	O	E	S	G	P	G	L	V	K	P	S	T	L	S	T	T	C	T	T	G	S	G	L	T	S	T	S	G	V	Y	V	W	R	O	P	P	60				
Db	14	M	K	H	L	T	F	L	L	V	A	A	P	R	W	L	S	O	V	L	S	O	V	L	O	E	S	G	P	G	L	V	K	P	S	T	L	S	T	T	C	T	T	G	S	G	L	T	S	T	S	G	V	Y	W	S	W	I	R	O	P	P	73
QY	61	G	K	G	L	E	W	G	I	V	A	G	G	T	T	N	S	A	L	M	S	R	L	T	I	S	K	D	T	S	K	N	O	V	L	S	K	L	S	V	T	A	A	D	T	A	V	Y	C	A	R	G	P	P	H	120							
Db	74	G	K	G	L	E	W	I	V	A	G	T	T	N	S	A	L	M	S	R	L	T	I	S	K	D	T	S	K	N	O	V	L	S	K	L	S	V	T	A	A	D	T	A	V	Y	C	A	R	G	P	P	H	133									
QY	121	A	M	M	K	R	G	I	A	N	D	Y	G	Q	G	T	L	V	T	V	S	142																																									
Db	134	S	S	W	Y	D	Y	G	M	D	V	W	G	Q	T	T	V	T	V	S	155																																										

	Query Match	64.2%;	Score 476;	DB 2;	Length 147;
	Best Local Similarity	69.4%;	Pred. No.	5.5e-35;	
	Matches 100; Conservative	12;	Mismatches	26;	Gaps      2;
QY	1	MAVLVLFCLVAFPSCVLSSOVQLQESGPGLVKPSQTLSLCTVTSGFSLTGYGVV--WVRQ	58		
Dd		: :     :			
Dd	8	MKLHWFLLLAAPRWLVLSQLQJESGPGLVKPSETLSLTCTVSGGISISSYYGWIRQ	67		
QY	59	PPKGLEWLGVTWAGGTITNNYSALMSRLTISKDTSKNOVSLKLSVVTAADTAVYYCARGP	118		
Dd		: :   : :   :   :   :   :   :   :   :   :   :			
Dd	68	PPKGGLEWIGSYISGSTYNFSCLKSRVTLSDVTSKNQSFSLKSSTAAATDPTAVYYCAR--	125		
QY	119	PHAMMKRGYAMDYGWGOTTLTVTSSS	142		
Dd		::			
Dd	126 --PLDMFGELFDYWGGOTTLTVTSS	147			

Search completed: May 7, 2002, 12:02:00  
Job time: 163 sec

